

In the Drawings:

Please replace FIG. 2-1 to 2-8 with replacement drawings FIG. 2-1 to 2-8.

REMARKS

Claims 1-28 and 30-43 were pending prior to entering the amendments.

The Amendments

The Table at pages 43 and 44 is amended to insert SEQ ID NOs.

At page 45, an obvious typographic error of “figure 5” is amended to “figure 2;” there is no figure 5 in the application and the text refers to the frameshift peptide of Figure 2.

Claims 1-43 are cancelled. New Claims 44-79 are added.

Claim 44 is supported by FIG. 2-1 and 2-2.

Claim 45 is supported by original Claim 3(d), page 8, lines 27-29, page 10, line 27 to page 11, line 5.

Claim 46 is supported by page 11, lines 8-11.

Claim 47 is supported by FIG. 2-2, TAF1b (-1).

Claim 48 is supported by FIG. 2-2, TAF1b (+1).

Claim 49 is supported by FIG. 2-1, HT001 (-1).

Claim 50 is supported by FIG. 2-1, HT001 (+1).

Claims 51-56 are supported by page 22, lines 17-18.

Claims 57-62 are supported by page 34, lines 11-16.

Claim 63 is supported by original Claims 18, 24, and 30, FIG. 2-1, FIG. 2-2, page 22, lines 17-18.

Claim 64 is supported by original Claim 3(d), page 8, lines 27-29, page 10, line 27 to page 11, line 5.

Claim 65 is supported by page 11, lines 8-11.

Claim 66 is supported by FIG. 2-2, TAF1b (-1).

Claim 67 is supported by FIG. 2-2, TAF1b (+1).

Claim 68 is supported by FIG. 2-1, HT001 (-1).

Claim 69 is supported by FIG. 2-1, HT001 (+1).

Claim 70 is supported by FIG. 2-1, TGFbRII (-1).

Claim 71 is supported by FIG. 2-1, TGFbRII (+1).

Claim 72 is supported by original Claims 18, 24, and 30; FIGs. 2-1 and 2-2; and page 34, lines 11-16.

Claim 73 is supported by original Claim 3(d), page 8, lines 27-29, page 10, line 27 to page 11, line 5.

Claim 74 is supported by FIG. 2-2, TAF1b (-1).

Claim 75 is supported by FIG. 2-2, TAF1b (+1).

Claim 76 is supported by FIG. 2-1, HT001 (-1).

Claim 77 is supported by FIG. 2-1, HT001 (+1).

Claim 78 is supported by FIG. 2-1, TGFbRII (-1).

Claim 79 is supported by FIG. 2-1, TGFbRII (+1).

The amendments in the drawings (FIGs. 2-1 to 2-8) are to insert sequence ID numbers. A marked copy of the drawings which shows the changes are included.

No new matter is added in any of the amendment. The Examiner is requested to enter the amendments.

Election/Restriction

Claims 3, 4, 11, 17, 30 and 31 were examined.

New Claims 40-50 correspond to the invention of Claim 3. New Claims 51-56 correspond to the invention of Claim 11. New claims 57-62 correspond to the invention of Claim 17. New Claims 63-69 correspond to the invention of Claim 30 (a).

New Claim 70-79 correspond to the elected invention, i.e., the combination of at least three polypeptides HT001, GGFBR2, and TAF1B (see Restriction Requirement at page 4, Group I, dated January 11, 2008, and Response to Restriction Requirement dated July 9, 2008).

The Response

35 U.S.C. §101 Rejection

Claims 3 and 4 are rejected under 35 U.S.C. 101. Claims 3-4 are cancelled.

New Claim 44 recites an isolated frameshift polypeptide. Therefore, the §101 Rejection should be withdrawn.

Claim Objections

Claims 4 and 31 are objected to under 37 CFR 1.75(c), as being of improper dependent form. Claims 4 and 31 are cancelled.

35 U.S.C. § 112, First Paragraph, Rejection – Written Description

Claims 3, 4, 11, 17, 30, and 31 are rejected under 35 U.S.C. 112, first paragraph, as allegedly failing to comply with the written description requirement for the following reasons:

Claims 3, 4, 11, 17, 30, and 31 are cancelled.

New Claims 44-79 are directed to frameshift polypeptide TAF1b (-1) ORF, TAF1b (+1) ORF, TAF1b (-2) ORF, HT001 (-1) ORF, HT001 (+1) ORF, HT001 (-2) ORF, TGFbRII (-1) ORF, TGFbRII (+1) ORF, and TGFbRII (-2). Each of the sequences is identified in FIGs. 2-1 and 2-2.

Therefore, the written description rejection should be withdrawn.

35 U.S.C. § 102(b) Rejection

Claims 3, 4, 11, 17, 30, and 31 are rejected under 35 U.S.C. 102(b) as being anticipated by Yang et al (Molecular and Cellular Biology, November 1996, 16(11):6603-6616). The rejection is traversed.

Yang et al. disclose that GCN3, GCD7 and GCD2 are regulatory domains in the guanine nucleotide exchange factor eIF2B. These proteins do not have any relationship to the subject matter of the present application. Furthermore, Yang et al. do not disclose the amino acid sequences of the claimed frameshift polypeptides of SEQ ID Nos: 2, 3, 20, 21, and 117-120.

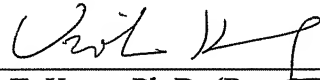
Therefore, the 102(b) rejection should be withdrawn.

CONCLUSION

Applicants believe that the application is now in good and proper condition for allowance.
Early notification of allowance is earnestly solicited.

Respectfully submitted,

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Enclosures: Replacement Drawings and Marked-Up Drawings

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FIG. 2-1

HT001**wt ORF (SEQ ID NO: 1)**

MQRPNNAHRISQPIRQIIYGLLLNASPHLDKTSWNALPPQPLAFSEVERINKNIRTSIIDAVELAKDHSLSRLTELSLRRRQMLLETALKV
KQTILEPIPTSLKLPVAVSCYWLQHTETKAKLHHLQSLLLTMLVGPLIAIINSPGKEELQEDGAKMLYAEFQVRVKAQTRLGTRLDLDTAHI
FCQWQSCLQMGMVLYNQLLSTPLPEPDLTRLVSGSLVHGLCQQLLASTSVESLLSICPEAKQLEYLFNATRSYAPAEIFLPKGRSNSK
KKRQKKQNTSCSKNRGRRTTAHTKCWYEGNNRFGLLMVENLEEHSSEASNIE

(-1) ORF (SEQ ID NO: 2)

MQRPNNAHRISQPIRQIIYGLLLNASPHLDKTSWNALPPQPLAFSEVERINKNIRTSIIDAVELAKDHSLSRLTELSLRRRQMLLETALKV
KQTILEPIPTSLKLPVAVSCYWLQHTETKAKLHHLQSLLLTMLVGPLIAIINSPGKEELQEDGAKMLYAEFQVRVKAQTRLGTRLDLDTAHI
FCQWQSCLQMGMVLYNQLLSTPLPEPDLTRLVSGSLVHGLCQQLLASTSVESLLSICPEAKQLEYLFNATRSYAPAEIFLPKGRSNSK
KKGRRNRIPAVLRTEGEPLHTPSVGMRETTGLGC

(+1)/(-2) ORF (SEQ ID NO: 3/118)

MQRPNNAHRISQPIRQIIYGLLLNASPHLDKTSWNALPPQPLAFSEVERINKNIRTSIIDAVELAKDHSLSRLTELSLRRRQMLLETALKV
KQTILEPIPTSLKLPVAVSCYWLQHTETKAKLHHLQSLLLTMLVGPLIAIINSPGKEELQEDGAKMLYAEFQVRVKAQTRLGTRLDLDTAHI
FCQWQSCLQMGMVLYNQLLSTPLPEPDLTRLVSGSLVHGLCQQLLASTSVESLLSICPEAKQLEYLFNATRSYAPAEIFLPKGRSNSK
KK(K)AEETEYQLF

U79260**wt ORF (SEQ ID NO: 4)**

MGHPRAIQPSVFFSPYDVHFLLYPIRCPYLKIGRFHIKLGKHLFLFSFLFFFETQSHSVTRLECSGTISAHCNLCPLGSSNSPASASRV
AGTAGTCRRAQLIFVFLAEMGFHHVGRDGLDNLVIHPPRSPKALGLQA

(-1) ORF (SEQ ID NO: 5)

MGHPRAIQPSVFFSPYDVHFLLYPIRCPYLKIGRFHIKLGKHLFLFSFLFFFLRHSLTSPGWSAVARSRLTATSASQVQVILLPQPPEW
LGLQARAAAPS

(+1)/(-2) ORF (SEQ ID NO: 6)

MGHPRAIQPSVFFSPYDVHFLLYPIRCPYLKIGRFHIKLGKHLFLFSFLFFF(F)

PTHL3**(wt) ORF (SEQ ID NO: 7)**

MQRRLVQQWSVAVFLLSYAVPSCGRSVEGLSRRLKRAVSEHQLLHDKGKSIQDLRRRFFLHHLIAEHTAEIRATSEVSPNSKPSNPNT
KNHPVRFGSDDEGRYLTQETNKVETYKEQPLKTPGKKKKGKPGKRKEQEKKRRRTRSAWLDSGVTGSGLEGDHLSDTSTTSLELD
SRTALLWGLKKKKENNRTHHMQLMISLFKSPLLLL

(-1) ORF (SEQ ID NO: 8)

MQRRLVQQWSVAVFLLSYAVPSCGRSVEGLSRRLKRAVSEHQLLHDKGKSIQDLRRRFFLHHLIAEHTAEIRATSEVSPNSKPSNPNT
KNHPVRFGSDDEGRYLTQETNKVETYKEQPLKTPGKKKKGKPGKRKEQEKKRRRTRSAWLDSGVTGSGLEGDHLSDTSTTSLELD
SRTALLWGLKKKKRKTTEEHIICN

(+1)/(-2) ORF (SEQ ID NO: 9)

MQRRLVQQWSVAVFLLSYAVPSCGRSVEGLSRRLKRAVSEHQLLHDKGKSIQDLRRRFFLHHLIAEHTAEIRATSEVSPNSKPSNPNT
KNHPVRFGSDDEGRYLTQETNKVETYKEQPLKTPGKKKKGKPGKRKEQEKKRRRTRSAWLDSGVTGSGLEGDHLSDTSTTSLELD
SRTALLWGLKKK(K)GKQQKNTSYATNDLII

TGFbRII**(wt) (SEQ ID NO: 10)**

MGRGLLRGLWPLHIVLWTRIASTIPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDFVRFSTCDNQKSCMSNCSITSICEKPQEVCAV
WRKNDENITLETVCHDPKLPYHDFILEDAAAPKCMKEKKKPGETFFMCSCSSDECNDNIIFSEEYNTSNPDLLLVIQVGTGISLLPPLG
VAISVIIIFCYRVNRQQLSSTWETGKTRKLMFSEHCAILEDSDSDISSTCANNINHNTELLPIELDTLVGKGRFAEVYKAKLKQNTS
EQFETVAVKIFPYEEYASWKTEKDIFSDINLKHENILQFLTAEERKTELKQYWLITAFHAKGNLQEYLTRHVISWEDLRKLGSLLARGI
AHLHSDHTPCGRPKMPIVHRDLNSSNVLKNDLTCCLCDFGLSLRLDPTLSVDDLANSGQVGTARYMAPEVLESRMNLENAESFKQT
DVYSMALVLWEMTSRCNAVGEVKDYEPFPGSKVREHPCVESMKDNVLRDRGRPEIPSWFLNHQGIQMVCELTTECWDHDPPEARLT
AQCVAERFSELEHLDRLSGRSCSEEKIPEDGSLNTTK

(-1) ORF (SEQ ID NO: 11)

MGRGLLRGLWPLHIVLWTRIASTIPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDFVRFSTCDNQKSCMSNCSITSICEKPQEVCAV
WRKNDENITLETVCHDPKLPYHDFILEDAAAPKCMKEKKSLVRLSSCVPALMSAMTTSSSQKNITPAILTCC

(+1)/(-2) ORF (SEQ ID NO: 12/119)

MGRGLLRGLWPLHIVLWTRIASTIPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDFVRFSTCDNQKSCMSNCSITSICEKPQEVCAV
WRKNDENITLETVCHDPKLPYHDFILEDAAAPKCMKEKK(K)AW

MACS**(wt) ORF (SEQ ID NO: 13)**

MGAQFSKTAAGGAAAERPGEAAVASSPSKANGQENGHVKNVNGDASPAEAESGAKEELQANGSAPAADKEEPAAGSGAASPSS
AEKGEPAAAAAEPAGASPVKEEAPAEGEAAEPGSATAAEGEAAASASTSSPKAEDGATPSPSNETPKKKKKRFSFKKSFKLSGFS
FKKNKKEAGEGGEAEAPAAEGGKDEAAGGAAAAAAEAGAASGEQAAAPGEEAAAGEEGAAGGDPQEAQKQEAQVAPEKPPASDE
TKAAEEPSKVEEKKAEAEAGASAAACEAPSAAGPGAPPEQEAAPAEPPAAAAASSACAAPSQEAQPECSPEAPPAAEAE

(-1) ORF (SEQ ID NO: 14)

MGAQFSKTAAGGAAAERPGEAAVASSPSKANGQENGHVKNVNGDASPAEAESGAKEELQANGSAPAADKEEPAAGSGAASPSS
AEKGEPAAAAAEPAGASPVKEEAPAEGEAAEPGSATAAEGEAAASASTSSPKAEDGATPSPSNETPKKKRSAFPRSRLSS

(+1)/(-2) ORF (SEQ ID NO: 15)

FIG. 2-2

MGAQFSKTAAGAAAERPGEAAVASSPSKANGQENGHVKNVDASPAAAESGAKEELQANGSAPAADKEEPAAAGSGAASPSS
 AEKGEPAAAAAEPAGASPVEKEAPAEGEAAEPGSATAAEGEAASASSTSSPKAEDGATPSPSNETPKKK(K)EALFLQEVFQAERL
LLQEEQEGGWRRR

TCF-4

(wt)ORF (Seq 10 NO: 16)

MPQLNGGGGDDLGADELISFKDEGEQEEKSSENSAERDLADVKSSLVNESETNQNSSSDSEARRPPPPRSESFRDKSRESLEE
 AKRQDGGFLFKGPPYPGYPFIMIPDLTSPYLPNGSLSPARTYLQMKWPLLDVQAGSLQSRQALKDARSPSPAHIVSNKVPVQHPHH
 VHPLTPLITYSNEHFTPGNPPPHLPADVDPKTGIPRPPHPPDISPYPLSPGTGQIPHLPLGWLVPQQGQPVYPITGGFRHPYPTALT
 VNASVSRFPPHMPVPHHTLHTTGIPHPAIVTPTVKQESSQSDVGSLSHSSKHQDSKKEEEKKKPHIKPLNAFMYMKEMRAKVVAEC
 TLKESAAINQILGRRWHALSREEQAKYYELARKERQLHMQLYPGWSARDNYGKKKKRKRDKQPGETNEHSECFLNPCLSLPPITDLS
 APKKCRARFGLDQQNNWCGPCRRKKKCVRYIQGEGSCLSPSSDGLSDSPSPNLLGSPPRDAKSQTEQTQPLSLSLKPDPLAH
 LSMMPPPPALLAEATHKASALCPNGALDLPAAALQPAAPSSSIAQPSTSWLHSHSSLAGTQPQPLSLVTKSLE

(-1)ORF (Seq 10 NO: 17)

MPQLNGGGGDDLGADELISFKDEGEQEEKSSENSAERDLADVKSSLVNESETNQNSSSDSEARRPPPPRSESFRDKSRESLEE
 AKRQDGGFLFKGPPYPGYPFIMIPDLTSPYLPNGSLSPARTYLQMKWPLLDVQAGSLQSRQALKDARSPSPAHIVSNKVPVQHPHH
 VHPLTPLITYSNEHFTPGNPPPHLPADVDPKTGIPRPPHPPDISPYPLSPGTGQIPHLPLGWLVPQQGQPVYPITGGFRHPYPTALT
 VNASVSRFPPHMPVPHHTLHTTGIPHPAIVTPTVKQESSQSDVGSLSHSSKHQDSKKEEEKKKPHIKPLNAFMYMKEMRAKVVAEC
 TLKESAAINQILGRRWHALSREEQAKYYELARKERQLHMQLYPGWSARDNYGKKKKRKRDKQPGETNEHSECFLNPCLSLPPITDLS
 APKKCRARFGLDQQNNWCGPCRRKKKSAFATYKVKAAASAHLQMEAY

(+1)/(-2)ORF (Seq 10 NO: 18)

MPQLNGGGGDDLGADELISFKDEGEQEEKSSENSAERDLADVKSSLVNESETNQNSSSDSEARRPPPPRSESFRDKSRESLEE
 AKRQDGGFLFKGPPYPGYPFIMIPDLTSPYLPNGSLSPARTYLQMKWPLLDVQAGSLQSRQALKDARSPSPAHIVSNKVPVQHPHH
 VHPLTPLITYSNEHFTPGNPPPHLPADVDPKTGIPRPPHPPDISPYPLSPGTGQIPHLPLGWLVPQQGQPVYPITGGFRHPYPTALT
 VNASVSRFPPHMPVPHHTLHTTGIPHPAIVTPTVKQESSQSDVGSLSHSSKHQDSKKEEEKKKPHIKPLNAFMYMKEMRAKVVAEC
 TLKESAAINQILGRRWHALSREEQAKYYELARKERQLHMQLYPGWSARDNYGKKKKRKRDKQPGETNEHSECFLNPCLSLPPITDLS
 APKKCRARFGLDQQNNWCGPCRRKK(K)VRLHTR

TAF1b

(wt)ORF (Seq 10 NO: 19)

IPAFAGTVLQPFPEAALATRVTPAVEAAPRLDLEEEEFKERCTQCAAVSWGLTDEGKYCTSCHNVTERYQEVNTNDLIPNT
 QIKALNRGLKKKNNTKEGWDWYVCEGFQYILYQQAELKNLGVGPGLKNDVLHNFWKRYLQKSKQAYCKNPVYTTGRKPTVLEDNL
 SHSDWASEPELLSDVSCPPFLESQAESQSDIHRKPPFVSKASQSETSVCSGSLDGVESQKKEGIVKMTMPQTLAFCYLSLLWQ
 REAITLSDLLRFVEEDHIPYINAFQHFPEQMPLYGRDRGIFGIESWPDYEDYKKTIEVGTFLDLPRFPDITEDCYLHPNLCMKYLMV
 LPDEMHSLTCHVVKMTGMGEVDFTFDPIAKMAKAVKYDVQAVAIIVVLKLLFLMDSDSEWLSNLAEKHNEKNKKDKPWDFRKY
 YQIMKKADEKKQKWEEARAKYLWKSEKPLYYSFVDKPVAYKKREMVNLQKQFSTLVDSTATAGKSPSSQFNWTEEDTDRTC
 FHGHSLOQVYLKEKGQSLTKNSLYWLSTQKFCRW

(-1)ORF (Seq 10 NO: 20)

IPAFAGTVLQPFPEAALATRVTPAVEAAPRLDLEEEEFKERCTQCAAVSWGLTDEGKYCTSCHNVTERYQEVNTNDLIPNT
 QIKALNRGLKKKTILKKAGIGMCVKVSSIFFINKQKP

(+1)/(-2)ORF (Seq 10 NO: 21/120)

IPAFAGTVLQPFPEAALATRVTPAVEAAPRLDLEEEEFKERCTQCAAVSWGLTDEGKYCTSCHNVTERYQEVNTNDLIPNT
 QIKALNRGLKKK(K)QY

AC-1

(wt)ORF (Seq 10 NO: 22)

MDTQKQIHKTHNSKNQFFTIFFLSVEFGKEGTRKNFYLLLSIGHYGRKSRRADLTADTADKTEPECFAASWTFDPNPSVTVSGAHS
 TAVHQ

(-1)ORF (Seq 10 NO: 23)

MDTQKQIHKTHNSKNQFFTIFFSCQLNLGRKEHAKITFFFFQLDMDGNPGETLLELQTLQIKSQSNALLPAGPLTQTPV

(+1)/(-2)ORF (Seq 10 NO: 24)

MDTQKQIHKTHNSKNQFFTIFF(F)PVS

Sec63

(wt)ORF (Seq 10 NO: 25)

MAGQQFYDDSGNTFFYFLTSFVGLVIPATYYLWPRDQNAEQIRLKNIRKVYGRCMWYRLRLKPQPNIIPTVKIVLLAGWALFLFL
 AYKVSKTREYQEYNPYEVLNLDPGATVAEIKKQYRLLSLKYHPDKGGDEVFMFRIAKAYAALTDEESRKNWEEFGNPDGPQATSF
 GIALPAWVVDQKNSILVLLVYGLAFMVLPPVVGSWWYRSIRYSGDQILRTTQIYTYFYKTRNMDMKRLIMVLGASEFDPQYNKDAT
 SRPTDNILIPQLIREIGSINLKKNEPPLTCPYSLKARVLLSLHARMKIPETLEEDQQFMLKKCPALLQEMVNVICQLIVMARNREEREFR
 APTLASLNCMKLSQMAVQGLQQFKSPLLQLPHIEEDNLRRVSNHKKYKIKTIQDLVSLKESDRHTLLHFLEDEKYEEMAVLGSFPY
 VTMDIKSQVLDDSDSNITVGSVLTVLVLTQRTMAEVEFEKEQSICAAEEQPAEDGQGETNKNRTKGGWQKQSKGPKKTAKSKKKK
 PLKKKPTPVLLPQSKQKQKQKQANGVVGNEAAVKEDEEEVSDKGSDEEEETNRDSQSEKDDGSDRDSREQDEKQNKDDEAEW
 QELQQSIQRKERALLETSKITHPVYSLYFPEEKQEWWWLYIADRKEQTLISMPYHVCTLKDTEEVELKFPAPGKPGNYQYTVFLRSD
 SYMGLDQIKPLKLEVHEAKVPENHPQWDTAIEGDEDQEDSEGFEDSFEEDDEEDDD

(-1) 9er A-Repeat (Seq 10 NO: 26)

MAGQQFYDDSGNTFFYFLTSFVGLVIPATYYLWPRDQNAEQIRLKNIRKVYGRCMWYRLRLKPQPNIIPTVKIVLLAGWALFLFL
 AYKVSKTREYQEYNPYEVLNLDPGATVAEIKKQYRLLSLKYHPDKGGDEVFMFRIAKAYAALTDEESRKNWEEFGNPDGPQATSF
 GIALPAWVVDQKNSILVLLVYGLAFMVLPPVVGSWWYRSIRYSGDQILRTTQIYTYFYKTRNMDMKRLIMVLGASEFDPQYNKDAT
 SRPTDNILIPQLIREIGSINLKKNEPPLTCPYSLKARVLLSLHARMKIPETLEEDQQFMLKKCPALLQEMVNVICQLIVMARNREEREFR
 APTLASLNCMKLSQMAVQGLQQFKSPLLQLPHIEEDNLRRVSNHKKYKIKTIQDLVSLKESDRHTLLHFLEDEKYEEMAVLGSFPY
 VTMDIKSQVLDDSDSNITVGSVLTVLVLTQRTMAEVEFEKEQSICAAEEQPAEDGQGETNKNRTKGGWQKQSKGPKKTAKSKKKR

L

FIG. 2-3

(+1)/(-2) 9er A-Repeat (SEQ ID NO: 27)

MAGQQFQYDDSGNTFFYFLTSFVGLVIPATYYLWPRDQNAEQIRLKNIRKVYGRCMWYRLRLLPQPNIIPTVKKIVLLAGWALFLFL
 AYKVSKTREYQEYNPYEVLNLDPGATVAEIKKQYRLLSLKYHPDKGGDEVFMFRIAKAYAALTDEESRKNWEEFGNPDGPQATSF
 GIALPAWIVDQKNSILVLLVYGLAFMVILPVVVGSWWYRSIRYSGDQILIRTTQIYTYFVYKTRNMDMKRLIMVLGASEFDPQYNKDAT
 SRPTDNILIPQLIREIGSINLKKNEPPLTCPYSLKARVLLLSHLARMKIPETLEEDQQFMLKKCPALLQEMVNVICQLIVMARNREEREFR
 APTLASLENCMKLSQMAVQGLQQFKSPLLQLPHIEEDNLRVSNHKKYKIKTIQDLVSLKESDRHTLLHFEDEKYEEMAVLGSFPY
 VTMDIKSQVLDDSDSNITVGSVLTVLVKLTRQTMAEVFEKEQSICAAEEQPAEDGQGETNKNRTKGGWQQ
 KSKGPKKTAKSKK(K)ETFKKKTYTCAITTVKATETKAGKWSRWE

(-1) 10er A-Repeat (SEQ ID NO: 28)

MAGQQFQYDDSGNTFFYFLTSFVGLVIPATYYLWPRDQNAEQIRLKNIRKVYGRCMWYRLRLLPQPNIIPTVKKIVLLAGWALFLFL
 AYKVSKTREYQEYNPYEVLNLDPGATVAEIKKQYRLLSLKYHPDKGGDEVFMFRIAKAYAALTDEESRKNWEEFGNPDGPQATSF
 GIALPAWIVDQKNSILVLLVYGLAFMVILPVVVGSWWYRSIRYSGDQILIRTTQIYTYFVYKTRNMDMKRLIMVLGASEFDPQYNKDAT
 SRPTDNILIPQLIREIGSINLKKNEPPLTCPYSLKARVLLLSHLARMKIPETLEEDQQFMLKKCPALLQEMVNVICQLIVMARNREEREFR
 APTLASLENCMKLSQMAVQGLQQFKSPLLQLPHIEEDNLRVSNHKKYKIKTIQDLVSLKESDRHTLLHFEDEKYEEMAVLGSFPY
 VTMDIKSQVLDDSDSNITVGSVLTVLVKLTRQTMAEVFEKEQSICAAEEQPAEDGQGETNKNRTKGGWQQ
 KSKGPKKTAKSKKKKPLK(K)NHLHCYYHSQSNRNKSRQMESLGMKLQ

(+1)/(-2) 10er A-Repeat (SEQ ID NO: 29)

MAGQQFQYDDSGNTFFYFLTSFVGLVIPATYYLWPRDQNAEQIRLKNIRKVYGRCMWYRLRLLPQPNIIPTVKKIVLLAGWALFLFL
 AYKVSKTREYQEYNPYEVLNLDPGATVAEIKKQYRLLSLKYHPDKGGDEVFMFRIAKAYAALTDEESRKNWEEFGNPDGPQATSF
 GIALPAWIVDQKNSILVLLVYGLAFMVILPVVVGSWWYRSIRYSGDQILIRTTQIYTYFVYKTRNMDMKRLIMVLGASEFDPQYNKDAT
 SRPTDNILIPQLIREIGSINLKKNEPPLTCPYSLKARVLLLSHLARMKIPETLEEDQQFMLKKCPALLQEMVNVICQLIVMARNREEREFR
 APTLASLENCMKLSQMAVQGLQQFKSPLLQLPHIEEDNLRVSNHKKYKIKTIQDLVSLKESDRHTLLHFEDEKYEEMAVLGSFPY
 VTMDIKSQVLDDSDSNITVGSVLTVLVKLTRQTMAEVFEKEQSICAAEEQPAEDGQGETNKNRTKGGWQQ
 KSKGPKKTAKSKKKKPLK(K)TYTCAITTVKATETKAGKWSRWE

Caspase 5**(wt)ORF (SEQ ID NO: 30)**

MFKGILQSGLDNFVINHMLKNNVAGQTSIQTLVPNTDQKSTSVKKDNHKKKTKVMLEYLGKDVHGVFNLYLAKHDVLTKEEEKKKYY
 DAKIEDKALILVDSLKRNRVAHQMFQTLLNMDQKITSVKPLQIEAGPPESAESTNILKCPREEFLRLCKKNHDEIYPIKKREDRRRLA
 LIICNTKFDLHLPARNGAHYDIVGMKRLQLGLGYTVVDEKNLTARDMESVLRFAFAARPEHKSSDSTFLVLMHSGILEGICGTAHKKKKP
 VLLYDTIFQIFNNRCLSLKDKPKVIIVQACRGEKHGELWVRDSPASLAVISSQSENLEADSVCKIHEEKDFIAFCSSSTPHNVSWDR
 TRGSIFITELITCFQKYSCCCHLMEIFRKVQKSFEVPOAKAQMPPTIERATLTRDFYLFPGN

(-1)ORF (SEQ ID NO: 31)

MFKGILQSGLDNFVINHMLKNNVAGQTSIQTLVPNTDQKSTSVKKDNHKKKQLRCWNTWAKMFFMVFLIHWQNTMF

(+1)/(-2)ORF (SEQ ID NO: 32)

MFKGILQSGLDNFVINHMLKNNVAGQTSIQTLVPNTDQKSTSVKKDNHKK(K)NS

AIM2**(wt)ORF (SEQ ID NO: 33)**

MESKYKEILLTGLDNITDEELDRFKFFLSDEFNIATGKLHTANRIQVATLMIQNAGAVSAVMKTIRIFQKLNMYLLAKRLQEEKEKVDKQ
 YKSVTKPKPLSQAEMSPAASAAIRNDVAKQRAAPKVSPHVKEQKQMVAAQESIREGFQKRCLPVMVLKAKKPFTFETQEGKQEMF
 HATVATEKEFFVVKVFNTLLKDKFIPKRIIIARYYRHSGFLEVNSASRVLDAESDQKVNVPNLNIRKAGETPKINTLQTQPLGTIVNGLFV
 VQKVTEKKKILFDLSDNTGKMEVLGVRNEDTMCKKEGDKVRLTFFTLKNGEKLQLTSGVHSTIKVIKAKKK

(-1)ORF (SEQ ID NO: 34)

MESKYKEILLTGLDNITDEELDRFKFFLSDEFNIATGKLHTANRIQVATLMIQNAGAVSAVMKTIRIFQKLNMYLLAKRLQEEKEKVDKQ
 YKSVTKPKPLSQAEMSPAASAAIRNDVAKQRAAPKVSPHVKEQKQMVAAQESIREGFQKRCLPVMVLKAKKPFTFETQEGKQEMF
 HATVATEKEFFVVKVFNTLLKDKFIPKRIIIARYYRHSGFLEVNSASRVLDAESDQKVNVPNLNIRKAGETPKINTLQTQPLGTIVNGLFV
 VQKVTEKKKILFDLSDNTGKMEVLGVRNEDTMCKKEGDKVRLTFFTLKNGEKLQLTSGVHSTIKVIKAKKKHREVKRTNSSQLV

(+1)/(-2)ORF (SEQ ID NO: 35)

MESKYKEILLTGLDNITDEELDRFKFFLSDEFNIATGKLHTANRIQVATLMIQNAGAVSAVMKTIRIFQKLNMYLLAKRLQEEKEKVDKQ
 YKSVTKPKPLSQAEMSPAASAAIRNDVAKQRAAPKVSPHVKEQKQMVAAQESIREGFQKRCLPVMVLKAKKPFTFETQEGKQEMF
 HATVATEKEFFVVKVFNTLLKDKFIPKRIIIARYYRHSGFLEVNSASRVLDAESDQKVNVPNLNIRKAGETPKINTLQTQPLGTIVNGLFV
 VQKVTEKKKILFDLSDNTGKMEVLGVRNEDTMCKKEGDKVRLTFFTLKNGEKLQLTSGVHSTIKVIKAKK(K)NIEK

SLC23A1**(wt)ORF (SEQ ID NO: 36)**

MMGIGKNTTSKSMEAGSSTEGKYEDEAKHPAFFTLPVVINGGATSSGEQDNEDTELMAYTTENGIAEKSSLAETLDSTGSLDPQRS
 DMIYTIEDVPPWYLICIFGLQHYLTCFSGTIAVPFLLADAMCVGYDQWATSQLIGTIFFCVGITLLQTTFFGCRPLPFQTSASAFLAPARA
 ILSLDKWKCNNTDVSANGTAELLHTEHIWYPRIREIQGAIIMSSLIEVVIGLLGLPGALLKYIGPLTITPTVALIGLSGFQAAGERAGKHW
 GIAMLTIFLVLLFSQYARNVKFPLPIYKSKKGWTAAYKLQLFKMFPIILAILVSWLLCFITVTDVFPDSTKYGFYARTDARQGVLLVAPW
 FKVPYFQWGLPTVSAAGVIGMLSAYVASIIESIGDYYACARLSCAPPPPIHAINRGIFVEGLSCVLDGIFGTGKNGSTSSPNIGVLGITK
 VGSRRVIQCGAALMLALGMIGKFSALFASLPDPVLGALFCTLFGMTAVGLSNLQFIDLNSSRNLFVLGFSIFFGLVLPYLRQNPLVTGI
 TGIDQVLNVLLTTAMFVGCCVAFILDNTIPGTPEERGIRKWKKGVGKGNKSLDGMESYNLPFGMNIKKYRCFSYLPISPTFVGTYWK
 GLRKSNSRSDSDSQATG

(-1)ORF (SEQ ID NO: 37)

MMGIGKNTTSKSMEAGSSTEGKYEDEAKHPAFFTLPVVINGGATSSGEQDNEDTELMAYTTENGIAEKSSLAETLDSTGSLDPQRS
 DMIYTIEDVPPWYLICIFGLQHYLTCFSGTIAVPFLLADAMCVGYDQWATSQLIGTIFFCVGITLLQTTFFGCRPLPFQTSASAFLAPARA
 ILSLDKWKCNNTDVSANGTAELLHTEHIWYPRIREIQGAIIMSSLIEVVIGLLGLPGALLKYIGPLTITPTVALIGLSGFQAAGERAGKHW
 GIAMLTIFLVLLFSQYARNVKFPLPIYKSKKGWTAAYKLQLFKMFPIILAILVSWLLCFITVTDVFPDSTKYGFYARTDARQGVLLVAPW
 FKVPYFQWGLPTVSAAGVIGMLSAYVASIIESIGDYYACARLSCAPPPPISTQ

(+1)/(-2)ORF (SEQ ID NO: 38)

FIG. 2-4

MMGIGKNTTSSKMEAGSSTEGKYEDEAKHPAFFTLPVVINGGATSSGEQDNEDTELMAYTTENGIAEKSSLAETLDSTGSLDPQRS
 DMIYTTIEDVPPWYLCLFLGLQHYLTCSGSIAPVFLADAMCVGYDQWATSQLIGITFFCVGITTLLQTTFGCRLPLFQTSFAFLAPARA
 ILSLDKWKCNNTDVSANGTAELLHTEHIWYPRIREIQGAIIMSSLIEVVIGLLGLPGALLKYIGPLTITPTVALIGLSGFQAAGERAGKHW
 GIAMLTIFLVLLFSQYARNVKFPLPIYKSKKGWTAAYKLQLFKMFPIILALVSWLLCFITVTVDVFPDSTKYGFYARTDARQGVLVAPW
 FKVPYPFQWGLPTVSAAGVIGMLSAAVASIIESIGDYYACARLSCAPP

(P)HPRNKQGNFRGRPLLS

ABCF1

(wt)ORF (SEQ ID NO: 39)

MPKAPKQQPPEPEWIGDGESTSPSPDKVVKKGKKDKKIKKTFFEEELAVEDKQAGEEEKVLKEKEQQQQQQQQQKKKRDTRKGRR
 KKDVDDDGEEKELMERLKKLSVPTSDEEDEVPAKPRGGKKTGGNVFAALIQDQSEEEEEEEKHPPKPAKPEKNRINKAVSEEQQ
 PALKGKKGKEEKSKGAKPQNKFAALDNEEDKEEEIIEKEPPKQGGKEKAKKAEQMEYERQVASLKAANAENDFSVQAEMSSR
 QAMLENASDIKLEKFSISAHGKELFVNADLYIVAGRRYGLVGPNGKGKTTLLKHIANRALSIPPNIIDVLLCEQEVVADETPAVQAVLRAD
 TKRLKLEEEERRLQGQLEQDDTAAERLEKVEELRATGAAAAEAKARRILAGLGFDPQMQRNPTQKFSGGWRMRVSLARALFMEP
 TLLMLDEPTNHLDLNNAVIWLNLYLQGWRTLLIVSHDQGLDDVCTDIIHLDAQRLHYRGNMTFKKMYQQQKQKELLKQYKQEKKL
 KELKAGGKSTKQAEKQTKALTRKQKQKRRKNQDEESQEAPELLKRPKEYTVRFTFPDPPPLSPPVLGLHGVTFGYQGQKPLFKNL
 DFGIDMDSRICIVGPNVGVKSTLLLLLTGKLTPTHGEMRKNHRLKIGFFNQQAQQLRMEETPTTEYLQRGFNLQPYQDARKCLGRFGLE
 SHAHTIQICKLSGGQKARVFAELACREPDVLILDEPTNNDIESIDALGEAINEYKGAIVVSHDARLITETNCQLVWVEEQSVSQIDG
 DFEDYKREVLALGEVMSRPRE

(-1)ORF (SEQ ID NO: 40)

MPKAPKQQPPEPEWIGDGESTSPSPDKVVKKGKKDKKIKKTFFEEELAVEDKQAGEEEKVLKEKEQQQQQQQQQKKKSEIPEKAGGR
RMWMMMEKRKSSWSVLRSSQCQVMRRMKYPPQNPAGRKPVRVVMFLQ

(+1)/(-2)ORF (SEQ ID NO: 41)

MPKAPKQQPPEPEWIGDGESTSPSPDKVVKKGKKDKKIKKTFFEEELAVEDKQAGEEEKVLKEKEQQQQQQQQQKK(K)ARYPKRQA
EEGCG

HSPC259

(wt)ORF (SEQ ID NO: 42)

SPDYFPQISSQGTVEK
 MEKIFISSSTKAEKGISPFAPINTQAPPEKGKEAVVQEPERSWFQTKKEERKKEKIAKALQEFDLALRGKKRKKKFMKDAKKKGEMT
 AEERSQFEILKAQMFAERLAKRNRRAKRARAMPEEEEPVRGPAKKQKQGGKSVFDEELTNTSKKALKQYRAGPSFEERKQLGLPHQR
 RGGNFKSNPDTRGGSSCRGLKKFMGAALKSLPCGKSSWLVLCLFSICLKKKQKQKTTLWCGGMVRSYFPHVCQSPFLISFHMILT
 NGSIFGKRE

(-1)ORF (SEQ ID NO: 43)

MEKIFISSSTKAEKGISPFAPINTQAPPEKGKEAVVQEPERSWFQTKKEERKKEKIAKALQEFDLALRGKKRKKKFMKDAKKKGEMT
 AEERSQFEILKAQMFAERLAKRNRRAKRARAMPEEEEPVRGPAKKQKQGGKSVFDEELTNTSKKALKQYRAGPSFEERKQLGLPHQR
 RGGNFKSNPDTRGGSSCRGLKKFMGAALKSLPCGKSSWLVLCLFSICLKKNKNKKQHFGVWWWYVAIFLSMSVNLPS

(+1)/(-2)ORF (SEQ ID NO: 44)

MEKIFISSSTKAEKGISPFAPINTQAPPEKGKEAVVQEPERSWFQTKKEERKKEKIAKALQEFDLALRGKKRKKKFMKDAKKKGEMT
 AEERSQFEILKAQMFAERLAKRNRRAKRARAMPEEEEPVRGPAKKQKQGGKSVFDEELTNTSKKALKQYRAGPSFEERKQLGLPHQR
 RGGNFKSNPDTRGGSSCRGLKKFMGAALKSLPCGKSSWLVLCLFSICLKK(K)TKTKNNTLWWWYGT

Bax

(wt)ORF (SEQ ID NO: 45)

MDGSGEQPRGGGPTSSEQIMKTGALLQGFIQDRAGRMGGEAPELALDPVPQDASTKKLSECLKRIGDELDSNMELQRMIAAVDTD
 SPREVFFRVAADMFSDGNFNWGRVVALFYFASKLVLKALCTKVPELIRTIMGWTLDFLRERLLGWIQDQGGWDGLLSYFGTPTWQT
 VTIFVAGVLTASLTWKKMG

(-1)ORF (SEQ ID NO: 46)

MDGSGEQPRGGGPTSSEQIMKTGALLQGFIQDRAGRMGGRHPSWPWTRCLMRPPRS

(+1)/(-2)ORF (SEQ ID NO: 47)

MDGSGEQPRGGGPTSSEQIMKTGALLQGFIQDRAGRMGG(G)GTRAGPGPGASGCVHQEAERVSQAHRGRTGQ

TCF6L1

(wt)ORF (SEQ ID NO: 48)

MAFLRSMWGLSALGRSGAELCTGCGSRLRSPFSFVYLPRWFSSVLASCPKPKPVSSYLRFSSKEQLPIFKAQNPDAKTTELIRRIAQR
 WRELPSKKKIYQDAYRAEWQVYKEEISRFEQLTPSQIMSLEKEIMDKHLKRKAMTKKKELTLGPKRPRSAYNVYVAERFQEAQ
 GDSPQEKLTQVKNWKNLSDSEKELYQHAKEDTRYHNEMKSWEEQMIIEVGRKDLLRRTIKKQRKYGAEEC

(-1)ORF (SEQ ID NO: 49)

MAFLRSMWGLSALGRSGAELCTGCGSRLRSPFSFVYLPRWFSSVLASCPKPKPVSSYLRFSSKEQLPIFKAQNPDAKTTELIRRIAQR
 WRELPSKKKIYQDAYRAEWQVYKEEISRFEQLTPSQIMSLEKEIMDKHLKRKAMTKKKK

(+1)/(-2)ORF (SEQ ID NO: 50)

MAFLRSMWGLSALGRSGAELCTGCGSRLRSPFSFVYLPRWFSSVLASCPKPKPVSSYLRFSSKEQLPIFKAQNPDAKTTELIRRIAQR
 WRELPSKKKIYQDAYRAEWQVYKEEISRFEQLTPSQIMSLEKEIMDKHLKRKAMTKKK(K)RVNTAWKTKTSFSL

FTL3L

(wt)ORF (SEQ ID NO: 51)

MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLKT
 VAGSKMQGLLERVNTIEHFVTKCAFQPPPSCLRFVQTNISRLQETSEQLVALKPWITRQNFSCRLELQCQPDSSSTLPPPWSPRPLE
 ATAPTAPQPLLLLLLPVGLLLAAWCLHWQRTTRRTPRPGEQVPPVPSQDLLLLVEH

(-1)ORF (SEQ ID NO: 52)

MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLKT
 VAGSKMQGLLERVNTIEHFVTKCAFQ
 PPPAVFASSRPTSPASCRPPSSWWVR

FIG. 2-5

(+1)/(-2)ORF (SEQ ID NO: 53)

MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLKT
VAGSKMQGLLERVNTIEHFVTKCAFQ
PP(P)QLSSLRPDQHLPPPAGDLRAAGGAELDHPELLVPVGAASAR

OGT

(wt)ORF (SEQ ID NO: 54)

MLQGHFWLVREGIMISPSSPPPNLFFFLQIFPFPFTSFPSHLLSLTPPKACYLKAJETQPNFAVAWSNLGCVFNAQGEIWLAIHFE
KAVTLDPNFLDAYINLGNVLKEARIFDRAVAAYLRALSLSPNHAVVHGNLACVYVEQGLIDLADTYRRAIELQPHFPDAYCNLANALKE
KGSVAEEDCYNTALRLOPTHADSLNNLANIKREQGNIIEAVRLYRKALEVFPEFAAAHSNLASVLQQQGLQEAALMHYKEAIRISPTF
ADAYSNMGNTLKEMQDVQGALQCYTRAIQINPAFADAHSNLASIHKDSGNIPEAIASYRTALKLPDFPDAYCNLAHCLQIVCDWTDY
DERMKKLVSIVADQLEKNRPLSVHPHHSMLYPLSHGFRKAIAERHGNLCLDKINVLHKPPYEHPKDLKLSGRLRVGYVSSDFGNHPT
SHLMQSIQGMHNPDKFEVFCYALSPDDGTNFRVKVMAEANHFIDLQIPCNCGKAADRIHQDGIHILVNMNGYTKGARNELFALRPAPI
QAMWLGYPGTSGALFMDYITDQETSPAEEVAEQYSEKLAYMPHTFFIGDHANMFPHLKKKKAVIDFKSNGHIYDNRIVLNGIDLKAFDLS
LPDVKIVKMKCPDGGDNADSSNTALNMPVIMNTIAEAVIEMINRGQIQITINGFSISNGLATTQINNKAATGEEVPTIIVTTRSQYGLP
CNGHTTGMDVLWAGTPMVTMPGETLASRVAASQLTCLGCELIANKRQEYEDIAVKLGTDLLEYLKKVRGKVVWQRISSPLFNTKQYT
MELERLYLQMWEEHYAAGNKPDMHKPVEVTEA

(-1)ORF (SEQ ID NO: 55)

MLQGHFWLVREGIMISPSSPPPNLFFSLYKFSFPFLPPFPPIFFH

(+1)/(-2)ORF (SEQ ID NO: 56)

MLQGHFWLVREGIMISPSSPPPNLFF(F)PFTNFPLSLYLLSLPSSFINPS

ELAVL3

(wt)ORF (SEQ ID NO: 57)

MESQVGGGPAGRPAQRPLLTGTNGATDDSKTNLIVNYPQNMTQDEFKSLFGSIGDIESCKLVRDKITGQSLGYGFVNYSNDPNADKA
INTLNLGLKLTQTKTIKVSYPARPSSASIRDANLYVSGLPKTMSSQKEMEQLFSQYGRITSRILVDQVTGVSRGVGFIRFDKRIEAEAAIKGLN
GQKPLGAREPITVKFANNPSQKTGQALLTHLYQSSARRYAGPLHHQTQRFRLDNLNLMAYAVKRFSPIADGMSGLAGVGLSGGAAG
GWCIFVYNLSPEDQSVLWQLFGPFGAVTNVKVIRDFTTNCKCKGFGFMTMTNYDEAAMAIASLNGYRLGQVRVLQVSFKTSKQHKHA

(-1)ORF (SEQ ID NO: 58)

MESQVGGARPAGLPNGHSLVQMEPLTTARPTSSSTTCPT

(+1)/(-2)ORF (SEQ ID NO: 59)

MESQVGG(G)PGRPACPTATPWYKWSH

MAC30X

(wt)ORF (SEQ ID NO: 60)

LFSHQVRVQAQPTDYGGSFTRRCVEWLLGLYFLSHIPITLFMDLQAVVPRELYPVEFRNLLKWYAKEFKDPLLQEPPAWFKSFLFCELV
FQLPFFPIATYAFKLGSKCWIRTPAIIYSVHTMTTLILILSTFLFEDFSKASGFKGQRPETLHERLTLVSVYAPYLLIPFILLIFMLRSPYYKY
EEKRKKK

(-1)ORF (SEQ ID NO: 61)

LFSHQVRVQAQPTDYGGSFTRRCVEWLLGLYFLSHIPITLFMDLQAVVPRELYPVEFRNLLKWYAKEFKDPLLQEPPAWFKSFLFCELV
FQLPFFPIATYAFKLGSKCWIRTPAIIYSVHTMTTLILILSTFLFEDFSKASGFKGQRPETLHERLTLVSVYAPYLLIPFILLIFMLRSPYYKY
EEKRKKKNEGNHWPVREMPGTGWLVLGYIQEHCEPTSSAAFETLAAMHKSKMVSGMTSNPHLLPFFFF

(+1)/(-2)ORF (SEQ ID NO: 62)

LFSHQVRVQAQPTDYGGSFTRRCVEWLLGLYFLSHIPITLFMDLQAVVPRELYPVEFRNLLKWYAKEFKDPLLQEPPAWFKSFLFCELV
FQLPFFPIATYAFKLGSKCWIRTPAIIYSVHTMTTLILILSTFLFEDFSKASGFKGQRPETLHERLTLVSVYAPYLLIPFILLIFMLRSPYYKY
EEKRKK(K)MKETTTGPG

SLC4A3

(wt)ORF (SEQ ID NO: 63)

MANGVIPIPPGGASPLPQVRVPLEEPPLSPDVEEEDDDLGKTLAVSRFGDLISKPPAWDPEKPSRSYSERDFEFHRHTSHHHTHPLSA
RLPPPHKLRLPPTSARHTRRKRKKEKTSAPPSEGTPIQEEGGAGVDEEEEEEEEEEGESEAEPVEPPPSGTPQKAKFSIGSDEDD
SPGLPGRAAVTKPLPSVGPHTDKSPQHSSSSSPRARASRLAGEKSRPWSPSASYDLRERLCPGSALGNPGGPEQQVPTDEAEAQ
MLGSADLDDMKSHRLEDNPGVRRHLVKKPSRTQGGGSGPSGLAPILRRKKKKKKLDRRPHEVFVELNELMLDRSQEPHWRETARW
IKFEEDVEEETERWGKPHVASLSFRSLELRLRTIAHGAALLDLEQTTLPGLAHVETMIVSDQIRPEDRASVLRTLLKHSHPNDDKDS
GFFPRNPSSSSMNSVLGNHHTPSPHGPDAVPTMADDLGEPAWPHDPDAKEKPLHMPGGDGHGKSLKLEKIPEDAEATVVL
VGCVPFLEQPAAAFVRLNEAVLLESVLEVPVPRFLVMLGPSHTSTDYHELGRSIATLMSDKLFHEAAYQADDRQDLSAISEFLDG
SIVIPPSEVEGRDLLRSVAAFQRELLRKRREREQTKVEMITTRGGYTAPGKELSELGGSEATPEDDPLRTGSGVFGGLVRDVRRRYP
HYPSDLRLDALHSQCVAALFYFAALSPAITFGGLGKEKTEGLMGVSELIVSTAVLGVFLSLLGAQPLLVGFSGPLLVFEEAFFKFCRA
QDLEYLTGRVWVGLWLVVFLVLAALVAEGSFLVRYISPFTQEIFAFLISLIFYETFYKLYKVFEHPLLPFPYPPGEAGLEGSAAGLEPNGS
ALPPTGPPSPRNQPNNTALLSLILMLGTFFIAFLRKFRNSRFLGGKARRIIGDFGIPISILVMVLVDYSITDTYTQKLTVPGLSVTSPDK
RSWFIPPLGSARPPPPWMMVAAPVALLVILIFMETQITALIVSQARRLLKSGSGFHLDLLIGSLGGLCGLFGLPWLTAAATVRSVTHV
NALVTMRTAIAPGDKPQIQEVREQRVTGVLIASLVGLSIVMGAVLRRIPLAVLFGFILYMGVTSLSGIQLSQRLLLILMPAKHHPEQPYVT
KVKTWRMHFLTQIQLGCIALLWVKSTAASLAFPLLLLLTVPLRHCLLPRLFQDRELQALDSEDAEPNFDGEDGQDEYNELHMPV

(-1)ORF (SEQ ID NO: 64)

MANGVIPIPPGGASPLPQVRVPLEEPPLSPDVEEEDDDLGKTLAVSRFGDLISKPPAWDPEKPSRSYSERDFEFHRHTSHHHTHPLSA
RLPPPHKLRLPPTSARHTRRKRKKEKTSAPPSEGTPIQEEGGAGVDEEEEEEEEEEGESEAEPVEPPPQGPHRQSSPLEVTRM
TVQASLGGLLSPSPCPRWAHTLTRAPSTPAAPPAGPGPPDSLGRKAGPGAHRPVMTCGSDCAQAVPWATQVVQSSRCQMRRR
PRCWLTQWT

(+1)/(-2)ORF (SEQ ID NO: 65)

MANGVIPIPPGGASPLPQVRVPLEEPPLSPDVEEEDDDLGKTLAVSRFGDLISKPPAWDPEKPSRSYSERDFEFHRHTSHHHTHPLSA
RLPPPHKLRLPPTSARHTRRKRKKEKTSAPPSEGTPIQEEGGAGVDEEEEEEEEEEGESEAEPVEPP(P)LRDPTEGKVLHWK

FIG. 2-6

PRKDC

(wt)ORF (SEQ ID NO: 66)

MAGSGAGVRCSLRLQETLSAADRCGAALAGHQLIRGLGQECVLS SSPAVLALQTSLVFSRDFGLLVFVRKSLNSIEFRECREEILKFL
CIFLEKMGQKIAPYSVEIKNTCTSVYTKDRAACKIPALDLLIKLLQTFRSSRLMDEFKIGELFSKFY GELALKKKIPDTVLEKVVYELLGLL
GEVHPSEMINNAENLFRALGELKTQMTSAVREP KLPVLAGCLKGLSSLLCNFTKSMEEPQTSREIFNFVLKAIRPQIDLKRYAVPSA
GLRLFALHASQFSTCLLDNYVSLFEVLLKWC AHTNVELKKAALSALESFLKQVSNMVAKNAEMHKNLQYFMEQFYGIIRNVDSNNKE
LSAIRGYGLFAGPCKVINAKDVFMYVELIQRCQKMF LTQTDTGDDR VYQMP SFLQSVASVLLYLDTVPEVYTPVLEHLVVMQIDSFP
QYSPKMQLVCCRAIVKVFALAAGPVL RNCISTVVHQGLIRICSKPVLPKGPESSESDHRASGEV RTGKWVPTYKYDYDLFRHLL
SSDQMMDSILADEAFFSVNSSSESLNHLLYDEFVKSVLKIVEKLDLTLEIQT VGEQENGDEAPGVWMIPTSDPAANLHPAKPKDFSAFI
NLVEFCREILPEKQAEFFEPWVYSFSYELILQSTR LPLISGFYKLLSITVRNAKKIKYFEGS

(-1)ORF (SEQ ID NO: 67)

MAGSGAGVRCSLRLQETLSAADRCGAALAGHQLIRGLGQECVLS SSPAVLALQTSLVFSRDFGLLVFVRKSLNSIEFRECREEILKFL
CIFLEKMGQKIAPYSVEIKNTCTSVYTKDRAACKIPALDLLIKLLQTFRSSRLMDEFKIGELFSKFY GELALKKK(Y)QIQF

(+) / (-2)ORF (SEQ ID NO: 68)

MAGSGAGVRCSLRLQETLSAADRCGAALAGHQLIRGLGQECVLS SSPAVLALQTSLVFSRDFGLLVFVRKSLNSIEFRECREEILKFL
CIFLEKMGQKIAPYSVEIKNTCTSVYTKDRAACKIPALDLLIKLLQTFRSSRLMDEFKIGELFSKFY GELALKK(K)NTRY SFRKS/

UVRAG

(wt)ORF (SEQ ID NO: 69)

MSASASVGGPVPQPPPGPAAALPPGSAARALHVELPSQQRRLRHLRNLIAARNIVNRNGHQLLD TYFTLHLCSTEKIYKEFYRSEVIKN
SLNPTWVRLDFGIMPDRLDTSVSCFVVKIWGGKENIYQLLIEWKVCLDGLKYL GQQIHARNQNEIIFGLNDGYYGAPFEHKGYSNAQK
TILLQVDQNCVRNSYDVFSLLRLHRAQCAIKQTQVT VQKIGKEIEEKLRLTSTSNELKKKSECLQKILVLQNELERQKKALGREVALLH
KQQALQDKGSFAEHLKLQKQESLNELRKECTAKRELFLKTNAQLTIRCRQLLS ELSYIYPIDLNEHKDYFVCGVKLPNS EDFQAK
DDGSI AVALGYTAHLVSMISFFLQVPLRYPPIHKGSRSSTIKDNINDKLTEKEREFP LYPKGGEKLQFDYGVYLLNKNI AQLRYQHGLGTP
DLRQTLPLNLKNFMEHGLMVRCDRHTTSSAIPV PKRQSSIFGGADVGFSGGIPSPDKGHRKRASSENERLQYKTPPPSYNSALAQPVT
TVPSMGETERKITSLSSSLDTSDFSKENKKKGEDLVGSLNGGHANVHPSQE QGEALSGHRATVNGTLLPSEQAGSASVQLPGEFH
PVSEALCCTVEQAEIIGLEAQVSPQVIS

(-1)ORF (SEQ ID NO: 70)

MSASASVGGPVPQPPPGPAAALPPGSAARALHVELPSQQRRLRHLRNLIAARNIVNRNGHQLLD TYFTLHLCSTEKIYKEFYRSEVIKN
SLNPTWVRLDFGIMPDRLDTSVSCFVVKIWGGKENIYQLLIEWKVCLDGLKYL GQQIHARNQNEIIFGLNDGYYGAPFEHKGYSNAQK
TILLQVDQNCVRNSYDVFSLLRLHRAQCAIKQTQVT VQKIGKEIEEKLRLTSTSNELKKK(V)NACS

(+) / (-2)ORF (SEQ ID NO: 71)

MSASASVGGPVPQPPPGPAAALPPGSAARALHVELPSQQRRLRHLRNLIAARNIVNRNGHQLLD TYFTLHLCSTEKIYKEFYRSEVIKN
SLNPTWVRLDFGIMPDRLDTSVSCFVVKIWGGKENIYQLLIEWKVCLDGLKYL GQQIHARNQNEIIFGLNDGYYGAPFEHKGYSNAQK
TILLQVDQNCVRNSYDVFSLLRLHRAQCAIKQTQVT VQKIGKEIEEKLRLTSTSNELKKK(K)

MSH3

(wt)ORF (SEQ ID NO: 72)

MSRRKPASGGLAASSAPARQAVLSRFFQSTGSLKSTSSSTGAADQVDPGAAAAAAAAAAAAAPPAPPAPAFPPQLPPHVATEIDRR
KKRPLENDGPVKKKVKVQKQEGGSDLGMSGNSEPKKCLRTNRVSKSLEKLKEFC CDSALPQSRVQTESLQERFAVL PKCTDFDDI
SLLHAKNAVSSEDSKRQINQKDTTLFDLSQFGSSNTSHENLQKTASKSANKRSKSIYTPLELQYIEMKQKHDAVLCVECGYKYRFFG
EDAEIAARELN IYCHLDHNFMTASIPTHRLFVHVRRLVAKGYKVG VVKQTETAALKAIGDNRSSLFSRKL TALYTKSTLIGEDVNPLIKLD
DAVNVDEIMTDTSTSYLLCISENKENVRDKKGNIFIGVGVQPATGEV VDFSQDSASRSELETRMSSLPQVE LLLPSALSEQTEALIH
RATSVSVQDDRI RVERMDNIYFEYSHAFQAVTEFYAKDTV DIKGSQIISGIVNLEKPVICSLAAIKYLKEFNLEKMLSKPENFKQLSSKM
EFMTINGTTLRNLEILQNQTD MKTKGSLLVVLDHTKTSFGRRRLKKWVTQPLLKLRINARLDAVSEVLHSESSVFGQIENHLRKL PDI
GRGLCSYHKKCSTQEFFLIVKTYLHLKSEFQAIPAVNSHIQSDLLRTVILEIPELLSPVEHYLKILNEQA AKVGDKTELFDLSDFLIKK
RKDEIQGVIDEIRMHQLKILKNPSAQYVTVSGQEFMIEIKNSAVSCIPTDWVKV GSTKAVSRFHS PFIVENYRHLNQLREQLVDCS
AEWLDLFLEKFSEHYHSLCKAVHHLATVDCIFSLAKVAKQGDYCRPTVQEERKIVIKNGRHPVIDVLLGEQDQYVPNNTDLS EDSESRVM
IITGPNNMGKSSYIKQVALITIMAQIGSYVPAEEATIGIVD GIFTRMGAADNIYKGRSTFMEELDTAEIIRKATSQS LVILDELGRGTSTH
DGAIAIAYATLEYFIRDVKS LTLFVTHYPPVCELEKNYSHQVGNYHMGFLVSEDESKLDPGTAEQVPDFVTFLYQITRGIAARSYGLNVA
KLADVPGEILKKAHKSKELEGLINTKRKRLKYFAKLWTMHN AQDLQKWTEEFNMEETQTSLLH

(-1)ORF (SEQ ID NO: 73)

MSRRKPASGGLAASSAPARQAVLSRFFQSTGSLKSTSSSTGAADQVDPGAAAAAAAAAAAAAPPAPPAPAFPPQLPPHVATEIDRR
KKRPLENDGPVKKKVKVQKQEGGSDLGMSGNSEPKKCLRTNRVSKSLEKLKEFC CDSALPQSRVQTESLQERFAVL PKCTDFDDI
SLLHAKNAVSSEDSKRQINQKDTTLFDLSQFGSSNTSHENLQKTASKSANKRSKSIYTPLELQYIEMKQKHDAVLCVECGYKYRFFG
EDAEIAARELN IYCHLDHNFMTASIPTHRLFVHVRRLVAKGYKVG VVKQTETAALKAIGDNRSSLFSRKL TALYTKSTLIGEDVNPLIKLD
DAVNVDEIMTDTSTSYLLCISENKENVRDKK(RATFLALWECSLPQARCLIVSR TLLVQS)

(+) / (-2)ORF (SEQ ID NO: 74)

MSRRKPASGGLAASSAPARQAVLSRFFQSTGSLKSTSSSTGAADQVDPGAAAAAAAAAAAAAPPAPPAPAFPPQLPPHVATEIDRR
KKRPLENDGPVKKKVKVQKQEGGSDLGMSGNSEPKKCLRTNRVSKSLEKLKEFC CDSALPQSRVQTESLQERFAVL PKCTDFDDI
SLLHAKNAVSSEDSKRQINQKDTTLFDLSQFGSSNTSHENLQKTASKSANKRSKSIYTPLELQYIEMKQKHDAVLCVECGYKYRFFG
EDAEIAARELN IYCHLDHNFMTASIPTHRLFVHVRRLVAKGYKVG VVKQTETAALKAIGDNRSSLFSRKL TALYTKSTLIGEDVNPLIKLD
DAVNVDEIMTDTSTSYLLCISENKENVRDKK(K)GQHFYWHCGSAACHRRGCV

ACVR2,

(wt) ORF (SEQ ID NO: 107)

MGAAAKLAFVFLISCSGA ILGRSETQEC LFFNANWEKD RTNQTGVEPC YGDKDKRRHC FATWKNISGS IEIVQGQCWL
DDINCYDRTD CVEKKSPEV YFCCCEGNMC NEKFSYFPEM EVTQPTSNPV TPKPPYYNIL LYSVLPLMLI AGIVICAFWV

FIG. 2-7

YRHHKMAYPP VLVPTQDPGP PPPSPLLGLK PLQLLEVkar GRFGCVWKAQ LLNEYVAVKI FPIQDKQSWQ NEYEVYSLPG
MKHENILQFI GAEKRGTSVD VDLWLITAFH EKGSLSDFLK ANVVSWNELC HIAETMARGL AYLHEDIPGL KDGHKPAISH
RDIKSKNVLL KNNLTACIAD FGLALKFEAG KSAGDTHGQV GTRRYMAPEV LEGAINFQRD AFLRIDMYAM GLVLWELASR
CTAADGPVDE YMLPFEEIEG QHPSLEDME VVHHKKRPV LRDYWQKHAG MAMLCETIEE CWDHDAEARL SAGCVGERIT
QMQRLTNIIT TEDIIVVTM VTNVDFPPKE SSL*

A8, Pos. 451: -1 ORF (Mut.rate 16.3%) (SEQ ID NO: 108)

MGAAAKLafa VFLISCSSGA ILGRSETQEC LFFNANWEKD RTNQTGVEPC YGDKDKRRHC FATWKNISGS IEIVKQGCWL
DDINCYDRTD CVEKKTALKY IFVAVRAICV MKSFLIFRRW KSHSPLQIQL HLSHPITTSC SIPWCHLC*

A8 Pos. 1476: -1 (Mut.rate 81.6%) (SEQ ID NO: 109)

MGAAAKLafa VFLISCSSGA ILGRSETQEC LFFNANWEKD RTNQTGVEPC YGDKDKRRHC FATWKNISGS IEIVKQGCWL
DDINCYDRTD CVEKKSPEV YFCCCEGNMC NEKFSYFPEM EVTQPTSNPV TPKPPYYNII LYSVLPLMI AGIVICAFWV
YRHHKMAYPP VLVPTQDPGP PPPSPLLGLK PLQLLEVkar GRFGCVWKAQ LLNEYVAVKI FPIQDKQSWQ NEYEVYSLPG
MKHENILQFI GAEKRGTSVD VDLWLITAFH EKGSLSDFLK ANVVSWNELC HIAETMARGL AYLHEDIPGL KDGHKPAISH
RDIKSKNVLL KNNLTACIAD FGLALKFEAG KSAGDTHGQV GTRRYMAPEV LEGAINFQRD AFLRIDMYAM GLVLWELASR
CTAADGPVDE YMLPFEEIEG QHPSLEDME VVHHKKRGLF*

FLJ11053, A11 Pos. 1695, Mut.rate 52.2%

wt ORF (SEQ ID NO: 110)

MVLRKLSKDD VTTLKAMQE FGTMCterDT ETVKGVLPYW PRIFCKISLD HRRVREATQ QAFEKLTlKV KKQLAPYLKS
LMGYWLMaQC DTYTPAAFAA KDAFEAAFP SKQPEAIaFC KDEITSVLQD HLIKETPDTL SDPQTVPEEE REAKFYRVVT
CSLLALKRLL CLLPDNElDS LEEKFKSLLS QNKFWKYGKH SVPQIRSAyF ELVSALCQRI PQLMKEEASK VSPSVLLSID
DSDPIVCPAL WEAVLYTLTT IEDCWLHVNA KKSVPFKLST VIREGGRGLA TVIYPYLLPF ISKLPHSITN PKLDFFKNFL
TSLVAGLSTE RTKTSSSESS AVISAFYECL RFIMQQNLGE EEIEQMLVND QLIPFIDAVL KDPGLQHGL QLNHLAETLSS
WEAKADTEKD EKTaHNLENV LIHFWERLSE ICVAKISEPE ADVESVLGVS NLLQVLQKPK SSLKSSKKKN GKVRFADEIL
ESNKENEKCV SSEGEKIEGW ELTTEPSLTH NSSGLLSPLR KKPLEDLVCK LADISINYVN ERKSEQHLRF LSTLLDSFSS
SRVFKMLLGD EKQSIvQAKP LEIAKLvQKN PAVQFLYQKL IGWLNEQDQK DFGFLVDILY SALRCCDNM

-1 ORF (SEQ ID NO: 111)

MVLRKLSKDD VTTLKAMQE FGTMCterDT ETVKGVLPYW PRIFCKISLD HRRVREATQ QAFEKLTlKV KKQLAPYLKS
LMGYWLMaQC DTYTPAAFAA KDAFEAAFP SKQPEAIaFC KDEITSVLQD HLIKETPDTL SDPQTVPEEE REAKFYRVVT
CSLLALKRLL CLLPDNElDS LEEKFKSLLS QNKFWKYGKH SVPQIRSAyF ELVSALCQRI PQLMKEEASK VSPSVLLSID
DSDPIVCPAL WEAVLYTLTT IEDCWLHVNA KKSVPFKLST VIREGGRGLA TVIYPYLLPF ISKLPHSITN PKLDFFKNFL
TSLVAGLSTE RTKTSSSESS AVISAFYECL RFIMQQNLGE EEIEQMLVND QLIPFIDAVL KDPGLQHGL QLNHLAETLSS
WEAKADTEKD EKTaHNLENV LIHFWERLSE ICVAKISEPE ADVESVLGVS NLLQVLQKPK SSLKSSKKKN VRLDLLMRYL
KAIKRMKNVYLQKERRLKAG N*

-2 ORF (SEQ ID NO: 112)

MVLRKLSKDD VTTLKAMQE FGTMCterDT ETVKGVLPYW PRIFCKISLD HRRVREATQ QAFEKLTlKV KKQLAPYLKS
LMGYWLMaQC DTYTPAAFAA KDAFEAAFP SKQPEAIaFC KDEITSVLQD HLIKETPDTL SDPQTVPEEE REAKFYRVVT
CSLLALKRLL CLLPDNElDS LEEKFKSLLS QNKFWKYGKH SVPQIRSAyF ELVSALCQRI PQLMKEEASK VSPSVLLSID
DSDPIVCPAL WEAVLYTLTT IEDCWLHVNA KKSVPFKLST VIREGGRGLA TVIYPYLLPF ISKLPHSITN PKLDFFKNFL
TSLVAGLSTE RTKTSSSESS AVISAFYECL RFIMQQNLGE EEIEQMLVND QLIPFIDAVL KDPGLQHGL QLNHLAETLSS
WEAKADTEKD EKTaHNLENV LIHFWERLSE ICVAKISEPE ADVESVLGVS NLLQVLQKPK SSLKSSKKKN W*

+1 ORF (SEQ ID NO: 113)

MVLRKLSKDD VTTLKAMQE FGTMCterDT ETVKGVLPYW PRIFCKISLD HRRVREATQ QAFEKLTlKV KKQLAPYLKS
LMGYWLMaQC DTYTPAAFAA KDAFEAAFP SKQPEAIaFC KDEITSVLQD HLIKETPDTL SDPQTVPEEE REAKFYRVVT
CSLLALKRLL CLLPDNElDS LEEKFKSLLS QNKFWKYGKH SVPQIRSAyF ELVSALCQRI PQLMKEEASK VSPSVLLSID
DSDPIVCPAL WEAVLYTLTT IEDCWLHVNA KKSVPFKLST VIREGGRGLA TVIYPYLLPF ISKLPHSITN PKLDFFKNFL
TSLVAGLSTE RTKTSSSESS AVISAFYECL RFIMQQNLGE EEIEQMLVND QLIPFIDAVL KDPGLQHGL QLNHLAETLSS
WEAKADTEKD EKTaHNLENV LIHFWERLSE ICVAKISEPE ADVESVLGVS NLLQVLQKPK SSLKSSKKKN W*

KIAA1052, A11 Pos. 689, Mut.rate 42.2%

Wt ORF (SEQ ID NO: 114)

MAGRPLRIGD QLVLEEDYDE TIYSEQEIL EFAREIGIDP IKEPELmWLA REGIVAPLPg EWKPCQDITG DIYFFNFANG
QSMWDHPCDE HYRSLVIER AKLSTSGAIK KKKKKKEKDD KKDRDPKSS LALGSSLAPV HVPLGGLAPL RGLVDTPPSA
LRGSQSVSLG SSVESGRQLG ELMLPSQGLK TSAYTKGLL SIYEDKTALS LLGLGEETNE EDEEESDNQS VHSSEPLRN
LHLDIGALGG DFEYEESLRT SQPEEKDVS LDSDAAGPPT PCKPSSPGAD SSLSSAVGKG RQGSARPGL PEKEENEKSE
PKICRNlVTP KADPTGSEPA KASEKEAPED TVDAGEEGSR REEAAKEPKK KASALEEGSS DASQEISE HMKEPQLSDS
IASDPKSFHG LDFGFRSRIS EHLLDvDVLs PVLGGACRQA QPLGIEDKD DSQSSQDELQ SKQSKGLEER YHRLSPPLPH
EERAQSPPRS LATEEEPPQG PEGQPEWKEA EELGEDSAAS LSLQLSLQRE QAPSPPAACE KGKEQHSQAE ELGPGQEEAE
DPEEKVAVSP TTPVSPPEVRS TEVPAPPEQL SEALKAMEE AVAQVLEQDQ RHLLSKQEK MQQLREKLCQ EEEEEILRLH
QQKEQSLSSL RERLQKAIEE EEARMREES QRLSWLRAQV QSSTQADEQ IRAEQEASLQ KLREELESQQ KAERASLEQK

FIG. 2-8

NRQMLEQLKE EIEASEKSEQ AALNAAKEKA LQQLREQLEG ERKEAVATLE KEHSAELERL CSSLEAKHRE WVSSLQKKIQ
 EAQQKEEAQL QKCLGQVEHR VHQKSYHVAG YEHELSSLLR EKRQEVEGEH ERRLDKMKKEE HQQVMAKARE QYEAEEKQR
 AELLGHLTGE LERLQRAHER ELETVRQEQH KRLEDLRRRH REQERKLQDL ELDLETRAKD VKARLALLEV QEETARREKQ
 QLLDVQRQVA LKSEEAATATH QQLEEAQKEH THLLQSNQQL REILDELQAR KLIKLESQVDL LQAQSQQLQK HFSSLEAEAQ
 KKQHLLREVT VEENNASPHF EPDLHIEDLR KSLGTNQTKE VSSLSQSKE DLYLDSLSSH NVWHLLSAEG VALRSAKEFL
 VQQTRSMRRR QTALKAAQQH WRHELASAE VAKDPPGIKA LEDMRKNLEK ETRHLDKMS AMRKGNLLK KKEEKLNLQLE
 SSLWEEASDE GTLGGSPKK AVTFDLSDMD SLSSSESSEF SPPHLDSTPS LTRKIHGLS HSLRQISSQL SSVLSILDSL
 NPQSPPLLA SMPAQLPPRD PKSTPTPTYY GSLARFSALS SATPTSTQWA WDSGQGPRLP SSVAAQTVDDF LLEKWRKYFP
 SGIPLLSNP TPLESRLLGYM SASEQLRLLQ HSHSQVPEAG STTFQGIIEA NRRWLERVKN DPRLPLFSST PKPKATLSLL
 QLGLDEHNRV KYYRF*

-1 ORF (SEQ ID NO: 115)

MAGRPLRIGD QLVLEEDYDE TYIPSEQEL EFAREIGIDP IKEPELMWLA REGIVAPLPG EWKPCQDITG DIYYNFNANG
 QSMWDHPCDE HYRSLVIQER AKLSTSGAIK KKKKKRKRKT RRTETPPKVR WPWVPH*

-2 ORF (SEQ ID NO: 116)

MAGRPLRIGD QLVLEEDYDE TYIPSEQEL EFAREIGIDP IKEPELMWLA REGIVAPLPG EWKPCQDITG DIYYNFNANG
 QSMWDHPCDE HYRSLVIQER AKLSTSGAIK KKKKKGKERQ EGQRPPQKEA GLGFLISPSS CSSWGPFSFT RSCGYPTLCS
SWISKREPG LSGVWTSARW THAAFTGSQD LCCLYKGSGLHI*

+1 ORF (SEQ ID NO: 117)

MAGRPLRIGD QLVLEEDYDE TYIPSEQEL EFAREIGIDP IKEPELMWLA REGIVAPLPG EWKPCQDITG DIYYNFNANG
 QSMWDHPCDE HYRSLVIQER AKLSTSGAIK KKKKKGKER QEGQRPPQKEA AGLGFLISPSS SCSSWGPFSF TRSCGYPTLC
SSWISKREPG ELSGVWTSARW THAAFTGSQ DLCLYKGSGLG LHI*